

SEQUENCE LISTING

Sub B1

(1) GENERAL INFORMATION:

- (i) APPLICANT: Meissner, Paul S.
Coleman, Timothy A.
- (ii) TITLE OF INVENTION: HUMAN CRIPTIN GROWTH FACTOR
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STEWART & OLSTEIN
 - (B) STREET: 6 Becker Farm Road
 - (C) CITY: Roseland
 - (D) STATE: N.J.
 - (E) COUNTRY: U.S.A
 - (F) ZIP: 07068
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/471,371
 - (B) FILING DATE: 06-JUN-1995
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ferraro, Gregory D.
 - (B) REGISTRATION NUMBER: 36,134
 - (C) REFERENCE/DOCKET NUMBER: 32580-455
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (201) 994-1700
 - (B) TELEFAX: (201) 994-1744

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 774 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 82..771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGCAGAAGA CTCTTCAAGA TTCAGCTTTC CTGGAACTG ATCTTCAATG CACTAAGAGA

60

AGGAGACTCT CAAACCCAAA A ATG ACC TGG AGG CAC CAT GTC AGG CTT CTG
Met Thr Trp Arg His His Val Arg Leu Leu
1 5 10

111

TTT ACG GTC AGT TTG GCA TTA CAG ATC ATC AAT TTG GGA AAC AGC TAT 159
Phe Thr Val Ser Leu Ala Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr 25

SAA AGA GAG AAA CAT AAC GGC GGT AGA GAG GAA GTC ACC AAG GTT GCC 207
Gln Arg Glu Lys His Asn Gly Gly Arg Glu Glu Val Thr Lys Val Ala 40

ACT CAG AAG CAC CGA CAG TCA CCG CTC AAC TGG ACC TCC AGT CAT TTC 255
Thr Gln Lys His Arg Gln Ser Pro Leu Asn Trp Thr Ser Ser His Phe 55

GGA GAG GTG ACT GGG AGC GCC GAG GGC TGG GGG CCG GAG GAG CCG CTC 303
Gly Glu Val Thr Gly Ser Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu 70

CCC TAC TCC CGG GCT TTC GGA GAG GGT GCG TCC GCG CGG CCG CGC TGC 351
Pro Tyr Ser Arg Ala Phe Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys 90

TGC AGG AAC GGC GGT ACC TGC GTG CTG GGC AGC TTC TGC GTG TGC CCG 399
Cys Arg Asn Gly Gly Thr Cys Val Leu Gly Ser Phe Cys Val Cys Pro 105

GCC CAC TTC ACC GGC CGC TAC TGC GAG CAT GAC CAG AGG CGC AGT GAA 447
Ala His Phe Thr Gly Arg Tyr Cys Glu His Asp Gln Arg Arg Ser Glu 120

TGC GGC GCC CTG GAG CAC GGA GCC TGG ACC CTC CGC GCC TGC CAC CTC 495
Cys Gly Ala Leu Glu His Gly Ala Trp Thr Leu Arg Ala Cys His Leu 135

TGC AGG TGC ATC TTC GGG GCC CTG CAC TGC CTC CCC CTC CAG ACG CCT 543
Cys Arg Cys Ile Phe Gly Ala Leu His Cys Leu Pro Leu Gln Thr Pro 150

GAC CGC TGT GAC CCG AAA GAC TTC CTG GCC TCC AAC GCT CAC GGG CCG 591
Asp Arg Cys Asp Pro Lys Asp Phe Leu Ala Ser His Ala His Gly Pro 170

AGC GCC GGG GGC GCG CCC AGC CTG CTA CTC TTG CTG CCC TGC GCA ACT 639
Ser Ala Gly Gly Ala Pro Ser Leu Leu Leu Leu Leu Pro Cys Ala Thr 185

CCT GCA CCG GCC TCC TGC GCC CGG ATG CGC CCG CGC ACC CTC GGT CCC 687
Pro Ala Pro Ala Ser Cys Ala Arg Met Arg Pro Arg Thr Leu Gly Pro 200

TGG TCC CTT CCG TCC TCC AGC GGG AGC GGC GCC CCT GCG GAA GGC CCG 735
Trp Ser Leu Pro Ser Ser Ser Gly Ser Gly Ala Pro Ala Glu Gly Arg 215

GAC TTG GGC ATC GCC TTT AAT TTT CTA TGT TGT AAA TAA 774
Asp Leu Gly Ile Ala Phe Asn Phe Leu Cys Cys Lys 230

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 230 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Trp Arg His His Val Arg Leu Leu Phe Thr Val Ser Leu Ala
1 5 10 15
Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr Gln Arg Glu Lys His Asn
20 25 30
Gly Gly Arg Glu Glu Val Thr Lys Val Ala Thr Gln Lys His Arg Gln
35 40 45
Ser Pro Leu Asn Trp Thr Ser Ser His Phe Gly Glu Val Thr Gly Ser
50 55 60
Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu Pro Tyr Ser Arg Ala Phe
65 70 75 80
Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys Cys Arg Asn Gly Gly Thr
85 90 95
Cys Val Leu Gly Ser Phe Cys Val Cys Pro Ala His Phe Thr Gly Arg
100 105 110
Tyr Cys Glu His Asp Gln Arg Arg Ser Glu Cys Gly Ala Leu Glu His
115 120 125
Gly Ala Trp Thr Leu Arg Ala Cys His Leu Cys Arg Cys Ile Phe Gly
130 135 140
Ala Leu His Cys Leu Pro Leu Gln Thr Pro Asp Arg Cys Asp Pro Lys
145 150 155 160
Asp Phe Leu Ala Ser His Ala His Gly Pro Ser Ala Gly Gly Ala Pro
165 170 175
Ser Leu Leu Leu Leu Leu Pro Cys Ala Thr Pro Ala Pro Ala Ser Cys
180 185 190
Ala Arg Met Arg Pro Arg Thr Leu Gly Pro Trp Ser Leu Pro Ser Ser
195 200 205
Ser Gly Ser Gly Ala Pro Ala Glu Gly Arg Asp Leu Gly Ile Ala Phe
210 215 220
Asn Phe Leu Cys Cys Lys
225 230

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACTCTTGAT CCAATTGGG AAACAGCTATC AAAGA

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TACAACTCTA GACTATTATT TACAACATAG AAAATTAAAG GC

42

- (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACTCTTGGAT CCGCCATCAT GACCTGGAGG CACCAT

36

- (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TACAACCAGC TGCTATTATT TACAACATAG

30

- (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 188 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Asp Cys Arg Lys Met Ala Arg Phe Ser Tyr Ser Val Ile Trp Ile
 1 5 10 15

Met	Ala	Ile	Ser	Lys	Val	Phe	Glu	Leu	Gly	Leu	Val	Ala	Gly	Leu	Gly
			20					25					30		
His	Gln	Glu	Phe	Ala	Arg	Pro	Ser	Arg	Gly	Tyr	Leu	Ala	Phe	Arg	Asp
		35					40					45			
Asp	Ser	Ile	Trp	Pro	Gln	Glu	Glu	Pro	Ala	Ile	Arg	Pro	Arg	Ser	Ser
	50					55					60				
Gln	Arg	Val	Pro	Pro	Met	Gly	Ile	Gln	His	Ser	Lys	Glu	Leu	Asn	Arg
65					70					75					80
Thr	Cys	Cys	Leu	Asn	Gly	Gly	Thr	Cys	Met	Leu	Gly	Ser	Phe	Cys	Ala
				85					90					95	
Cys	Pro	Pro	Ser	Phe	Tyr	Gly	Arg	Asn	Cys	Glu	His	Asp	Val	Arg	Lys
			100					105					110		
Glu	Asn	Cys	Gly	Ser	Val	Pro	His	Asp	Thr	Trp	Leu	Pro	Lys	Lys	Cys
		115					120					125			
Ser	Leu	Cys	Lys	Cys	Trp	His	Gly	Gln	Leu	Arg	Cys	Phe	Pro	Gln	Ala
	130					135					140				
Phe	Leu	Pro	Gly	Cys	Asp	Gly	Leu	Val	Met	Asp	Glu	His	Leu	Val	Ala
145					150					155					160
Ser	Arg	Thr	Pro	Glu	Leu	Pro	Pro	Ser	Ala	Arg	Thr	Thr	Thr	Phe	Met
				165					170					175	
Leu	Val	Gly	Ile	Cys	Leu	Ser	Ile	Gln	Ser	Tyr	Tyr				
			180					185							